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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Wed Jun 06 09:21:07 EDT 2007

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Application No: 10586312 Version No: 1.0

Input Set:**Output Set:**

Started: 2007-05-18 17:03:25.456
Finished: 2007-05-18 17:03:27.180
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 724 ms
Total Warnings: 32
Total Errors: 64
No. of SeqIDs Defined: 56
Actual SeqID Count: 56

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
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W 213	Artificial or Unknown found in <213> in SEQ ID (11)
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W 213	Artificial or Unknown found in <213> in SEQ ID (14)
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W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna

Input Set :

Output Set :

```
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E 336	Empty lines found between the proteins and the dna
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E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Jukka T. SALONEN et al.

<120> METHOD FOR DETECTING THE RISK OF CARDIOVASCULAR DISEASES SUCH AS ACUTE MYOCARDIAL INFARCTION AND CORONARY HEART DISEASE BY ANALYSING DEFENSIN

<130> 0933-0279PUS1

<140> 10586312

<141> 2007-05-18

<150> US 10/586,312

<151> 2006-07-14

<160> 56

<170> PatentIn version 3.1

<210> 1

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

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<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

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<210> 3

<211> 18

<212> DNA

<213> Artificial Sequence

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<210> 4
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

 <400> 4
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 <210> 5
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

 <400> 5
 ctgagtgtgc aggacgag 18

 <210> 6
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

 <400> 6
 cacattgcca aacacgat 18

 <210> 7
 <211> 736
 <212> DNA
 <213> Homo sapiens

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 caggctgact cctcactccc cacatatcca ctctgctct ccctcctgca ggtgacccca 180

 gccatgagga ccatcgccat ccttgctgcc attctcctgg tggccctgca ggcccaggct 240

 gagtcactcc aggaaagagc tgatgaggct acaaccaga agcagtctgg ggaagacaac 300

 caggaccttg ctatctcctt tgcaggaaat ggactctctg ctcttagaac ctcaggtagg 360

 agacatcaat cttgcacatc tgcaaaatct agaaaaaag gattggagaa aggatctgga 420

 gtcaagtgtg gaaagggtcta cctcacttga gtgactttac ttaatcttcc tggaccttga 480

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taagactttc agttccaaga tatttctgtg aaatttgcta cttttaagat agaaagacct 600
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caggctgact cctcactccc cacatatcca ctctgctct cctcctgca ggtgaccca 180
gccatgagga ccatcgccat ccttgctgcc attctcctgg tggccctgca ggcccaggct 240
gagtcactcc aggaaagagc tgatgaggct acaaccaga agcagtctgg ggaagacaac 300
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agacatcaat cttgcacatc tgcaaaatct agaaaaaag gattggagaa aggatctgga 420
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taagactttc agctccaaga tatttctgtg aaatttgcta cttttaagat agaaagagct 600
aactgacta gttctttgta gatctaaatg ggcagactta gttatataga gagtgtttta 660
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<220>
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<220>
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<210> 11
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<220>
<223> Description of Artificial Sequence: PCR primer

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<210> 12
<211> 20
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<220>
<223> Description of Artificial Sequence: PCR primer

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<210> 13
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<213> Artificial Sequence

<220>
<223> Snapshot primer

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<210> 15
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<220>
<223> Snapshot primer

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<223> Snapshot primer

<400> 16
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<210> 17
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<213> Artificial Sequence

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<213> Artificial Sequence

<220>
<223> Snapshot primer

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<210> 19
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<212> DNA
<213> Artificial Sequence

<220>

<223> Snapshot primer

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<210> 20
<211> 1344
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1344)
<223> Coding sequence for variant human ADRA2B gene

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15
gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg96
Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
202530
gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac144
Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
354045
ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc192
Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
505560
atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc240
Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65707580
cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc288
Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
859095
acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg336
Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
100105110
gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc384
Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
115120125
atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg432
Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
130135140
ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg480
Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
145150155160

cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc	528
Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser	
165 170 175	
agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac	576
Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr	
180 185 190	
ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg	624
Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg	
195 200 205	
gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac	672
Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp	
210 215 220	
cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg	720
His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val	
225 230 235 240	
gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag	768
Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys	
245 250 255	
gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc	816
Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro	
260 265 270	
agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt	864
Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val	
275 280 285	
tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag	912
Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu	
290 295 300	
gag gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc tca gct tgc	960
Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys	
305 310 315 320	
agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg gcc acc cta	1008
Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu	
325 330 335	
cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata ggt ggg cag	1056
Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln	
340 345 350	
tgg tgg cgt cga agg gcg cac gtg acc cgg gag aag cgc ttc acc ttc	1104
Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe	
355 360 365	
gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg ttc ccc ttc	1152
Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe	
370 375 380	
ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac tgc aag gtg	1200

Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
385 390 395 400

ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac tgc aac agc 1248
Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
405 410 415

tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt 1296
Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
420 425 430

gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg gcc tgg tga 1344
Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
435 440 445

<210> 21
<211> 447
<212> PRT
<213> Homo sapiens

<400> 21

Met Asp His Gln Asp Pro Tyr Ser Val Gln Ala Thr Ala Ala Ile Ala
1 5 10 15

Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
20 25 30

Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
35 40 45

Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
50 55 60

Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65 70 75 80

Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
85 90 95

Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
100 105 110

Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
115 120 125

Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
130 135 140

Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
145 150 155 160

Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
165 170 175

Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
180 185 190

Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
195 200 205

Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
210 215 220

His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
225 230 235 240

Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
245 250 255

Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
260 265 270

Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
275 280 285

Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
290 295 300

Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
305 310 315 320

Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
325 330 335

Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
340 345 350

Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
355 360 365

Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
370 375 380

Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
385 390 395 400

Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
405 410 415

Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
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Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
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<213> Homo sapiens

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<223> Coding sequence for human ADRA2B gene

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Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
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gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac 144

Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
35 40 45

ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc 192
Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
50 55 60

atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc 240
Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
65 70 75 80

cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc 288
Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
85 90 95

acc tcg tcc atc gtg